

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Goodwin, Raymond G.
Smith, Craig A.
Armitage, Richard J.
Gruss, Hans-Jurgen

(ii) TITLE OF INVENTION: Novel Cytokine That Binds CD30

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

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(D) STATE: Washington
(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/225,989
(B) FILING DATE: 12-APR-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/966,775
(B) FILING DATE: 27-OCT-1992
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 907,224
(B) FILING DATE: 01-JUL-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 899,660
(B) FILING DATE: 15-JUN-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 892,459
(B) FILING DATE: 02-JUN-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 889,717
(B) FILING DATE: 26-MAY-1992

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seese, Kathryn A.
(B) REGISTRATION NUMBER: 32,172
(C) REFERENCE/DOCKET NUMBER: 2804-E

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1788 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: huCD30

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	CGC	GTC	CTC	CTC	GCC	GCG	CTG	GGA	CTG	CTG	TTC	CTG	GGG	GCG	CTA	48
Met	Arg	Val	Leu	Leu	Ala	Ala	Leu	Gly	Leu	Leu	Phe	Leu	Gly	Ala	Leu	
1			5						10						15	
CGA	GCC	TTC	CCA	CAG	GAT	CGA	CCC	TTC	GAG	GAC	ACC	TGT	CAT	GGA	AAC	96
Arg	Ala	Phe	Pro	Gln	Asp	Arg	Pro	Phe	Glu	Asp	Thr	Cys	His	Gly	Asn	
			20					25					30			
CCC	AGC	CAC	TAC	TAT	GAC	AAG	GCT	GTC	AGG	AGG	TGC	TGT	TAC	CGC	TGC	144
Pro	Ser	His	Tyr	Tyr	Asp	Lys	Ala	Val	Arg	Arg	Cys	Cys	Tyr	Arg	Cys	
			35					40				45				
CCC	ATG	GGG	CTG	TTC	CCG	ACA	CAG	CAG	TGC	CCA	CAG	AGG	CCT	ACT	GAC	192
Pro	Met	Gly	Leu	Phe	Pro	Thr	Gln	Gln	Cys	Pro	Gln	Arg	Pro	Thr	Asp	
			50				55				60					
TGC	AGG	AAG	CAG	TGT	GAG	CCT	GAC	TAC	TAC	CTG	GAT	GAG	GCC	GAC	CGC	240
Cys	Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Asp	Arg	
			65				70			75			80			
TGT	ACA	GCC	TGC	GTG	ACT	TGT	TCT	CGA	GAT	GAC	CTC	GTG	GAG	AAG	ACG	288
Cys	Thr	Ala	Cys	Val	Thr	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	
			85				90						95			
CCG	TGT	GCA	TGG	AAC	TCC	TCC	CGT	GTC	TGC	GAA	TGT	CGA	CCC	GGC	ATG	336
Pro	Cys	Ala	Trp	Asn	Ser	Ser	Arg	Val	Cys	Glu	Cys	Arg	Pro	Gly	Met	
			100				105					110				
TTC	TGT	TCC	ACG	TCT	GCC	AAC	TCC	TGT	GCC	CGC	TGC	TTC	TTC	CAT	384	
Phe	Cys	Ser	Thr	Ser	Ala	Val	Asn	Ser	Cys	Ala	Arg	Cys	Phe	Phe	His	
			115				120				125					

TCT	GTC	TGT	CCG	GCA	GGG	ATG	ATT	GTC	AAG	TTC	CCA	GGC	ACG	GCG	CAG	432
Ser	Val	Cys	Pro	Ala	Gly	Met	Ile	Val	Lys	Phe	Pro	Gly	Thr	Ala	Gln	
130						135									140	
AAG	AAC	ACG	GTC	TGT	GAG	CCG	GCT	TCC	CCA	GGG	GTC	AGC	CCT	GCC	TGT	480
Lys	Asn	Thr	Val	Cys	Glu	Pro	Ala	Ser	Pro	Gly	Val	Ser	Pro	Ala	Cys	
145					150					155					160	
GCC	AGC	CCA	GAG	AAC	TGC	AAG	GAA	CCC	TCC	AGT	GGC	ACC	ATC	CCC	CAG	528
Ala	Ser	Pro	Glu	Asn	Cys	Lys	Glu	Pro	Ser	Ser	Gly	Thr	Ile	Pro	Gln	
					165				170						175	
GCC	AAG	CCC	ACC	CCG	GTG	TCC	CCA	GCA	ACC	TCC	AGT	GCC	AGC	ACC	ATG	576
Ala	Lys	Pro	Thr	Pro	Val	Ser	Pro	Ala	Thr	Ser	Ser	Ala	Ser	Thr	Met	
					180				185						190	
CCT	GTA	AGA	GGG	GGC	ACC	CGC	CTC	GCC	CAG	GAA	GCT	GCT	TCT	AAA	CTG	624
Pro	Val	Arg	Gly	Gly	Thr	Arg	Leu	Ala	Gln	Glu	Ala	Ala	Ser	Lys	Leu	
					195			200			205					
ACG	AGG	GCT	CCC	GAC	TCT	CCC	TCC	TCT	GTG	GGA	AGG	CCT	AGT	TCA	GAT	672
Thr	Arg	Ala	Pro	Asp	Ser	Pro	Ser	Ser	Val	Gly	Arg	Pro	Ser	Ser	Asp	
					210			215			220					
CCA	GGT	CTG	TCC	CCA	ACA	CAG	CCA	TGC	CCA	GAG	GGG	TCT	GGT	GAT	TGC	720
Pro	Gly	Leu	Ser	Pro	Thr	Gln	Pro	Cys	Pro	Glu	Gly	Ser	Gly	Asp	Cys	
					225			230		235					240	
AGA	AAG	CAG	TGT	GAG	CCC	GAC	TAC	TAC	CTG	GAC	GAG	GCC	GGC	CGC	TGC	768
Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Gly	Arg	Cys	
					245			250			255					
ACA	GCC	TGC	GTG	AGC	TGT	TCT	CGA	GAT	GAC	CTT	GTG	GAG	AAG	ACG	CCA	816
Thr	Ala	Cys	Val	Ser	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	Pro	
					260			265			270					
TGT	GCA	TGG	AAC	TCC	TCC	CGC	ACC	TGC	GAA	TGT	CGA	CCT	GGC	ATG	ATC	864
Cys	Ala	Trp	Asn	Ser	Ser	Arg	Thr	Cys	Glu	Cys	Arg	Pro	Gly	Met	Ile	
					275			280			285					
TGT	GCC	ACA	TCA	GCC	ACC	AAC	TCC	TGT	GCC	CGC	TGT	GTC	CCC	TAC	CCA	912
Cys	Ala	Thr	Ser	Ala	Thr	Asn	Ser	Cys	Ala	Arg	Cys	Val	Pro	Tyr	Pro	
					290			295			300					
ATC	TGT	GCA	GGA	GAG	ACG	GTC	ACC	AAG	CCC	CAG	GAT	ATG	GCT	GAG	AAG	960
Ile	Cys	Ala	Gly	Glu	Thr	Val	Thr	Lys	Pro	Gln	Asp	Met	Ala	Glu	Lys	
					305			310		315					320	
GAC	ACC	ACC	TTT	GAG	GCG	CCA	CCC	CTG	GGG	ACC	CAG	CCG	GAC	TGC	AAC	1008
Asp	Thr	Thr	Phe	Glu	Ala	Pro	Pro	Leu	Gly	Thr	Gln	Pro	Asp	Cys	Asn	
					325			330			335					
CCC	ACC	CCA	GAG	AAT	GGC	GAG	GCG	CCT	GCC	AGC	ACC	AGC	CCC	ACT	CAG	1056
Pro	Thr	Pro	Glu	Asn	Gly	Glu	Ala	Pro	Ala	Ser	Thr	Ser	Pro	Thr	Gln	
					340			345			350					
AGC	TTG	CTG	GTG	GAC	TCC	CAG	GCC	AGT	AAG	ACG	CTG	CCC	ATC	CCA	ACC	1104
Ser	Leu	Leu	Val	Asp	Ser	Gln	Ala	Ser	Lys	Thr	Leu	Pro	Ile	Pro	Thr	
					355			360			365					
AGC	GCT	CCC	GTC	GCT	CTC	TCC	ACG	GGG	AAG	CCC	GTC	GAT	GCA		1152	

Ser	Ala	Pro	Val	Ala	Leu	Ser	Ser	Thr	Gly	Lys	Pro	Val	Leu	Asp	Ala			
370						375					380							
GGG	CCA	GTG	CTC	TTC	TGG	GTG	ATC	CTG	GTG	TTG	GTT	GTG	GTG	GTC	GGC	1200		
Gly	Pro	Val	Leu	Phe	Trp	Val	Ile	Leu	Val	Leu	Val	Val	Val	Val	Gly			
385						390				395					400			
TCC	AGC	GCC	TTC	CTC	CTG	TGC	CAC	CGG	AGG	GCC	TGC	AGG	AAG	CGA	ATT	1248		
Ser	Ser	Ala	Phe	Leu	Leu	Cys	His	Arg	Arg	Ala	Cys	Arg	Lys	Arg	Ile			
							405		410					415				
CGG	CAG	AAG	CTC	CAC	CTG	TGC	TAC	CCG	GTC	CAG	ACC	TCC	CAG	CCC	AAG	1296		
Arg	Gln	Lys	Leu	His	Leu	Cys	Tyr	Pro	Val	Gln	Thr	Ser	Gln	Pro	Lys			
							420		425					430				
CTA	GAG	CTT	GTG	GAT	TCC	AGA	CCC	AGG	AGG	AGC	TCA	ACG	CAG	CTG	AGG	1344		
Leu	Glu	Leu	Val	Asp	Ser	Arg	Pro	Arg	Arg	Ser	Ser	Thr	Gln	Leu	Arg			
							435		440					445				
AGT	GGT	GCG	TCG	GTG	ACA	GAA	CCC	GTC	GCG	GAA	GAG	CGA	GGG	TTA	ATG	1392		
Ser	Gly	Ala	Ser	Val	Thr	Glu	Pro	Val	Ala	Glu	Glu	Arg	Gly	Leu	Met			
							450		455					460				
AGC	CAG	CCA	CTG	ATG	GAG	ACC	TGC	CAC	AGC	GTG	GGG	GCA	GCC	TAC	CTG	1440		
Ser	Gln	Pro	Leu	Met	Glu	Thr	Cys	His	Ser	Val	Gly	Ala	Ala	Tyr	Leu			
							465		470					475			480	
GAG	AGC	CTG	CCG	CTG	CAG	GAT	GCC	AGC	CCG	GCC	GGG	GGC	CCC	TCG	TCC	1488		
Glu	Ser	Leu	Pro	Leu	Gln	Asp	Ala	Ser	Pro	Ala	Gly	Gly	Pro	Ser	Ser			
							485		490					495				
CCC	AGG	GAC	CTT	CCT	GAG	CCC	CGG	GTG	TCC	ACG	GAG	CAC	ACC	AAT	AAC	1536		
Pro	Arg	Asp	Leu	Pro	Glu	Pro	Arg	Val	Ser	Thr	Glu	His	Thr	Asn	Asn			
							500		505					510				
AAG	ATT	GAG	AAA	ATC	TAC	ATC	ATG	AAG	GCT	GAC	ACC	GTG	ATC	GTG	GGG	1584		
Lys	Ile	Glu	Lys	Ile	Tyr	Ile	Met	Lys	Ala	Asp	Thr	Val	Ile	Val	Gly			
							515		520					525				
ACC	GTG	AAG	GCT	GAG	CTG	CCG	GAG	GGC	CGG	GGC	CTG	GCG	GGG	CCA	GCA	1632		
Thr	Val	Lys	Ala	Glu	Leu	Pro	Glu	Gly	Arg	Gly	Leu	Ala	Gly	Pro	Ala			
							530		535					540				
GAG	CCC	GAG	TTG	GAG	GAG	GAG	CTG	GAG	GCG	CAT	ACC	CCC	CAC	TAC		1680		
Glu	Pro	Glu	Leu	Glu	Glu	Glu	Leu	Glu	Ala	Asp	His	Thr	Pro	His	Tyr			
							545		550					555			560	
CCC	GAG	CAG	GAG	ACA	GAA	CCG	CCT	CTG	GGC	AGC	TGC	AGC	GAT	GTC	ATG	1728		
Pro	Glu	Gln	Glu	Thr	Glu	Pro	Pro	Leu	Gly	Ser	Cys	Ser	Asp	Val	Met			
							565		570					575				
CTC	TCA	GTG	GAA	GAG	GAA	GGG	AAA	GAA	GAC	CCC	TTG	CCC	ACA	GCT	GCC	1776		
Leu	Ser	Val	Glu	Glu	Glu	Gly	Lys	Glu	Asp	Pro	Leu	Pro	Thr	Ala	Ala			
							580		585					590				
TCT	GGA	AAG	TGA													1788		
Ser	Gly	Lys																
			595															

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 595 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu
1 5 10 15

Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn
20 25 30

Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys
35 40 45

Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp
50 55 60

Cys Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Asp Arg
65 70 75 80

Cys Thr Ala Cys Val Thr Cys Ser Arg Asp Asp Leu Val Glu Lys Thr
85 90 95

Pro Cys Ala Trp Asn Ser Ser Arg Val Cys Glu Cys Arg Pro Gly Met
100 105 110

Phe Cys Ser Thr Ser Ala Val Asn Ser Cys Ala Arg Cys Phe Phe His
115 120 125

Ser Val Cys Pro Ala Gly Met Ile Val Lys Phe Pro Gly Thr Ala Gln
130 135 140

Lys Asn Thr Val Cys Glu Pro Ala Ser Pro Gly Val Ser Pro Ala Cys
145 150 155 160

Ala Ser Pro Glu Asn Cys Lys Glu Pro Ser Ser Gly Thr Ile Pro Gln
165 170 175

Ala Lys Pro Thr Pro Val Ser Pro Ala Thr Ser Ser Ala Ser Thr Met
180 185 190

Pro Val Arg Gly Gly Thr Arg Leu Ala Gln Glu Ala Ala Ser Lys Leu
195 200 205

Thr Arg Ala Pro Asp Ser Pro Ser Ser Val Gly Arg Pro Ser Ser Asp
210 215 220

Pro Gly Leu Ser Pro Thr Gln Pro Cys Pro Glu Gly Ser Gly Asp Cys
225 230 235 240

Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Gly Arg Cys
245 250 255

Thr Ala Cys Val Ser Cys Ser Arg Asp Asp Leu Val Glu Lys Thr Pro
260 265 270

Cys Ala Trp Asn Ser Ser Arg Thr Cys Glu Cys Arg Pro Gly Met Ile
 275 280 285
 Cys Ala Thr Ser Ala Thr Asn Ser Cys Ala Arg Cys Val Pro Tyr Pro
 290 295 300
 Ile Cys Ala Gly Glu Thr Val Thr Lys Pro Gln Asp Met Ala Glu Lys
 305 310 315 320
 Asp Thr Thr Phe Glu Ala Pro Pro Leu Gly Thr Gln Pro Asp Cys Asn
 325 330 335
 Pro Thr Pro Glu Asn Gly Glu Ala Pro Ala Ser Thr Ser Pro Thr Gln
 340 345 350
 Ser Leu Leu Val Asp Ser Gln Ala Ser Lys Thr Leu Pro Ile Pro Thr
 355 360 365
 Ser Ala Pro Val Ala Leu Ser Ser Thr Gly Lys Pro Val Leu Asp Ala
 370 375 380
 Gly Pro Val Leu Phe Trp Val Ile Leu Val Leu Val Val Val Val Gly
 385 390 395 400
 Ser Ser Ala Phe Leu Leu Cys His Arg Arg Ala Cys Arg Lys Arg Ile
 405 410 415
 Arg Gln Lys Leu His Leu Cys Tyr Pro Val Gln Thr Ser Gln Pro Lys
 420 425 430
 Leu Glu Leu Val Asp Ser Arg Pro Arg Arg Ser Ser Thr Gln Leu Arg
 435 440 445
 Ser Gly Ala Ser Val Thr Glu Pro Val Ala Glu Glu Arg Gly Leu Met
 450 455 460
 Ser Gln Pro Leu Met Glu Thr Cys His Ser Val Gly Ala Ala Tyr Leu
 465 470 475 480
 Glu Ser Leu Pro Leu Gln Asp Ala Ser Pro Ala Gly Gly Pro Ser Ser
 485 490 495
 Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn
 500 505 510
 Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly
 515 520 525
 Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala
 530 535 540
 Glu Pro Glu Leu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr
 545 550 555 560
 Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met
 565 570 575
 Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala
 580 585 590
 Ser Gly Lys

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 699 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: hIgG1Fc

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAG CCC AGA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA	48
Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala	
1 5 10 15	
CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC	96
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro	
20 25 30	
AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG	144
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val	
35 40 45	
TG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG	192
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val	
50 55 60	
GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG	240
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln	
65 70 75 80	
TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG	288
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln	
85 90 95	
GAC TGG CTG AAT GGC AAG GAC TAC AAG TGC AAG GTC TCC AAC AAA GCC	336
Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala	
100 105 110	
CTC CCA GCC CCC ATG CAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC	384
Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro	
115 120 125	
CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC	432

Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	
130							135				140					
AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGG	480
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Arg	
145					150					155				160		
CAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	528
His	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	
							165		170				175			
AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	576
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	
							180		185			190				
AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	624
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	
						195		200			205					
TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	672
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	
						210		215			220					
AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA								699
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys									
					225		230									

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu	Pro	Arg	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	
1						5			10				15			
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	
						20			25			30				
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	
						35			40			45				
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	
						50			55			60				
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	
						65			70			75			80	
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	
						85			90			95				
Asp	Trp	Leu	Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	
						100			105			110				
Leu	Pro	Ala	Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	

115	120	125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr		
130	135	140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg		
145	150	155
His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr		
165	170	175
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr		
180	185	190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe		
195	200	205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys		
210	215	220
Ser Leu Ser Leu Ser Pro Gly Lys		
225	230	

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: muCD30-L
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GAG CCA GGG CTG CAA CAA GCA GGC AGC TGT GGG GCT CCT TCC CCT	48
Met Glu Pro Gly Leu Gln Gln Ala Gly Ser Cys Gly Ala Pro Ser Pro	
1 5 10 15	
GAC CCA GCC ATG CAG GTG CAG CCC GGC TCG GTA GCC AGC CCC TGG AGA	96
Asp Pro Ala Met Gln Val Gln Pro Gly Ser Val Ala Ser Pro Trp Arg	
20 25 30	
AGC ACG AGG CCC TGG AGA AGC ACA AGT CGC AGC TAC TTC TAC CTC AGC	144
Ser Thr Arg Pro Trp Arg Ser Thr Ser Arg Ser Tyr Phe Tyr Leu Ser	
35 40 45	
ACC ACC GCA CTG GTG TGC CTT GTT GTG GCA GTG GCG ATC ATT CTG GTA	192
Thr Thr Ala Leu Val Cys Leu Val Val Ala Val Ile Ile Leu Val	

50	55	60	
CTG GTA GTC CAG AAA AAG GAC TCC ACT CCA AAT ACA ACT GAG AAG GCC Leu Val Val Gln Lys Lys Asp Ser Thr Pro Asn Thr Thr Glu Lys Ala			240
65	70	75	80
CCC CTT AAA GGA GGA AAT TGC TCA GAG GAT CTC TTC TGT ACC CTG AAA Pro Leu Lys Gly Gly Asn Cys Ser Glu Asp Leu Phe Cys Thr Leu Lys			288
85	90		95
AGT ACT CCA TCC AAG AAG TCA TGG GCC TAC CTC CAA GTG TCA AAG CAT Ser Thr Pro Ser Lys Lys Ser Trp Ala Tyr Leu Gln Val Ser Lys His			336
100	105		110
CTC AAC AAT ACC AAA CTG TCA TGG AAC GAA GAT GGC ACC ATC CAC GGA Leu Asn Asn Thr Lys Leu Ser Trp Asn Glu Asp Gly Thr Ile His Gly			384
115	120		125
CTC ATA TAC CAG GAC GGG AAC CTG ATA GTC CAA TTC CCT GGC TTG TAC Leu Ile Tyr Gln Asp Gly Asn Leu Ile Val Gln Phe Pro Gly Leu Tyr			432
130	135		140
TTC ATC GTT TGC CAA CTG CAG TTC CTC GTG CAG TGC TCA AAT CAT TCT Phe Ile Val Cys Gln Leu Gln Phe Leu Val Gln Cys Ser Asn His Ser			480
145	150	155	160
GTG GAC CTG ACA TTG CAG CTC CTC ATC AAT TCC AAG ATC AAA AAG CAG Val Asp Leu Thr Leu Gln Leu Ile Asn Ser Lys Ile Lys Lys Gln			528
165	170		175
ACG TTG GTA ACA GTG TGT GAG TCT GGA GTT CAG AGT AAG AAC ATC TAC Thr Leu Val Thr Val Cys Glu Ser Gly Val Gln Ser Lys Asn Ile Tyr			576
180	185		190
CAG AAT CTC TCT CAG TTT TTG CTG CAT TAC TTA CAG GTC AAC TCT ACC Gln Asn Leu Ser Gln Phe Leu Leu His Tyr Leu Gln Val Asn Ser Thr			624
195	200		205
ATA TCA GTC AGG GTG GAT AAT TTC CAG TAT GTG GAT ACA AAC ACT TTC Ile Ser Val Arg Val Asp Asn Phe Gln Tyr Val Asp Thr Asn Thr Phe			672
210	215		220
CCT CTT GAT AAT GTG CTA TCC GTC TTC TTA TAT AGT AGC TCA GAC TGA Pro Leu Asp Asn Val Leu Ser Val Phe Leu Tyr Ser Ser Ser Asp			720
225	230	235	240

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Pro	Gly	Leu	Gln	Gln	Ala	Gly	Ser	Cys	Gly	Ala	Pro	Ser	Pro
1				5				10					15		

Asp	Pro	Ala	Met	Gln	Val	Gln	Pro	Gly	Ser	Val	Ala	Ser	Pro	Trp	Arg
			20					25						30	
Ser	Thr	Arg	Pro	Trp	Arg	Ser	Thr	Ser	Arg	Ser	Tyr	Phe	Tyr	Leu	Ser
		35					40					45			
Thr	Thr	Ala	Leu	Val	Cys	Leu	Val	Val	Ala	Ile	Ile	Leu	Val		
		50				55				60					
Leu	Val	Val	Gln	Lys	Lys	Asp	Ser	Thr	Pro	Asn	Thr	Thr	Glu	Lys	Ala
		65				70			75				80		
Pro	Leu	Lys	Gly	Gly	Asn	Cys	Ser	Glu	Asp	Leu	Phe	Cys	Thr	Leu	Lys
		85						90					95		
Ser	Thr	Pro	Ser	Lys	Lys	Ser	Trp	Ala	Tyr	Leu	Gln	Val	Ser	Lys	His
		100					105					110			
Leu	Asn	Asn	Thr	Lys	Leu	Ser	Trp	Asn	Glu	Asp	Gly	Thr	Ile	His	Gly
		115					120					125			
Leu	Ile	Tyr	Gln	Asp	Gly	Asn	Leu	Ile	Val	Gln	Phe	Pro	Gly	Leu	Tyr
		130				135			140						
Phe	Ile	Val	Cys	Gln	Leu	Gln	Phe	Leu	Val	Gln	Cys	Ser	Asn	His	Ser
		145				150			155				160		
Val	Asp	Leu	Thr	Leu	Gln	Leu	Leu	Ile	Asn	Ser	Lys	Ile	Lys	Lys	Gln
		165					170					175			
Thr	Leu	Val	Thr	Val	Cys	Glu	Ser	Gly	Val	Gln	Ser	Lys	Asn	Ile	Tyr
		180				185					190				
Gln	Asn	Leu	Ser	Gln	Phe	Leu	Leu	His	Tyr	Leu	Gln	Val	Asn	Ser	Thr
		195				200					205				
Ile	Ser	Val	Arg	Val	Asp	Asn	Phe	Gln	Tyr	Val	Asp	Thr	Asn	Thr	Phe
		210				215				220					
Pro	Leu	Asp	Asn	Val	Leu	Ser	Val	Phe	Leu	Tyr	Ser	Ser	Ser	Asp	
		225				230			235						

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 705 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: huCD30-L

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GAC CCA GGG CTG CAG CAA GCA CTC AAC GGA ATG GCC CCT CCT GGA Met Asp Pro Gly Leu Gln Gln Ala Leu Asn Gly Met Ala Pro Pro Gly	48
1 5 10 15	
GAC ACA GCC ATG CAT GTG CCG GCG GGC TCC GTG GCC AGC CAC CTG GGG Asp Thr Ala Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly	96
20 25 30	
ACC ACG AGC CGC AGC TAT TTC TAT TTG ACC ACA GCC ACT CTG GCT CTG Thr Thr Ser Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu	144
35 40 45	
TGC CTT GTC TTC ACG GTG GCC ACT ATT ATG GTG TTG GTC GTT CAG AGG Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg	192
50 55 60	
ACG GAC TCC ATT CCC AAC TCA CCT GAC AAC GTC CCC CTC AAA GGA GGA Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly	240
65 70 75 80	
AAT TGC TCA GAA GAC CTC TTA TGT ATC CTG AAA AGA GCT CCA TTC AAG Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys	288
85 90 95	
AAG TCA TGG GCC TAC CTC CAA GTG GCA AAG CAT CTA AAC AAA ACC AAG Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys	336
100 105 110	
TTG TCT TGG AAC AAA GAT GGC ATT CTC CAT GGA GTC AGA TAT CAG GAT Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp	384
115 120 125	
GGG AAT CTG GTG ATC CAA TTC CCT GGT TTG TAC TTC ATC ATT TGC CAA Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Ile Ile Cys Gln	432
130 135 140	
CTG CAG TTT CTT GTA CAA TGC CCA AAT AAT TCT GTC GAT CTG AAG TTG Leu Gln Phe Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu	480
145 150 155 160	
GAG CTT CTC ATC AAC AAG CAT ATC AAA AAA CAG GCC CTG GTG ACA GTG Glu Leu Leu Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val	528
165 170 175	
TGT GAG TCT GGA ATG CAA ACG AAA CAC GTA TAC CAG AAT CTC TCT CAA Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln	576
180 185 190	
TTC TTG CTG GAT TAC CTG CAG GTC AAC ACC ACC ATA TCA GTC AAT GTG Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val	624
195 200 205	
GAT ACA TTC CAG TAC ATA GAT ACA AGC ACC TTT CCT CTT GAG AAT GTG Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val	672
210 215 220	
TTG TCC ATC TTC TTA TAC AGT AAT TCA GAC TGA Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp	705

225

230

235

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Pro Gly Leu Gln Gln Ala Leu Asn Gly Met Ala Pro Pro Gly
1 5 10 15

Asp Thr Ala Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly
20 25 30

Thr Thr Ser Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu
35 40 45

Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg
50 55 60

Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly
65 70 75 80

Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys
85 90 95

Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys
100 105 110

Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp
115 120 125

Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln
130 135 140

Leu Gln Phe Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu
145 150 155 160

Glu Leu Leu Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val
165 170 175

Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln
180 185 190

Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val
195 200 205

Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val
210 215 220

Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp
225 230

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: 5' PCR Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATAGCGGCCG CCACCATGCG CGTCCTCCTC GCCGCGCTG

39

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: 3' PCR Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACAAGATCTG GGCTCCTTCC CCGTGGAGGA GAGAGCGAC

39

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: BGL II Adaptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCTGGCAA CGAAGGTACC ATGG

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: BGL II Adaptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCATGGTACC TTCTGTTGCCA

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: Upstream sequence

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG GGC TGT GGG GCT CCT TCC CCT GAC CCA GCC
Met Gly Cys Gly Ala Pro Ser Pro Asp Pro Ala
1 5 10

33

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Cys Gly Ala Pro Ser Pro Asp Pro Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: FLAG peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: Murine cDNA Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGATGCTTTG ACACATTG

17

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: Human cDNA Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCACCAAGAT TCCCCATC

17

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: muCD30-L

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG	CAG	GTG	CAG	CCC	GGC	TCG	GTA	GCC	AGC	CCC	TGG	AGA	AGC	ACG	AGG	48
Met	Gln	Val	Gln	Pro	Gly	Ser	Val	Ala	Ser	Pro	Trp	Arg	Ser	Thr	Arg	
1		5					10							15		
CCC	TGG	AGA	AGC	ACA	AGT	CGC	AGC	TAC	TTC	TAC	CTC	AGC	ACC	ACC	GCA	96
Pro	Trp	Arg	Ser	Thr	Ser	Arg	Ser	Tyr	Phe	Tyr	Leu	Ser	Thr	Thr	Ala	
20		25						25				30				
CTG	GTG	TGC	CTT	GTT	GTG	GCA	GTG	GCG	ATC	ATT	CTG	GTA	CTG	GTA	GTC	144
Leu	Val	Cys	Leu	Val	Val	Ala	Val	Ala	Ile	Ile	Leu	Val	Leu	Val	Val	
35						35		40			45					
CAG	AAA	AAG	GAC	TCC	ACT	CCA	AAT	ACA	ACT	GAG	AAG	GCC	CCC	CTT	AAA	192
Gln	Lys	Lys	Asp	Ser	Thr	Pro	Asn	Thr	Thr	Glu	Lys	Ala	Pro	Leu	Lys	
50		55					55			60						
GGA	GGA	AAT	TGC	TCA	GAG	GAT	CTC	TTC	TGT	ACC	CTG	AAA	AGT	ACT	CCA	240
Gly	Gly	Asn	Cys	Ser	Glu	Asp	Leu	Phe	Cys	Thr	Leu	Lys	Ser	Thr	Pro	
65		70					70		75			80				
TCC	AAG	AAG	TCA	TGG	GCC	TAC	CTC	CAA	GTG	TCA	AAG	CAT	CTC	AAC	AAT	288
Ser	Lys	Lys	Ser	Trp	Ala	Tyr	Leu	Gln	Val	Ser	Lys	His	Leu	Asn	Asn	
85		90					85		90			95				
ACC	AAA	CTG	TCA	TGG	AAC	GAA	GAT	GGC	ACC	ATC	CAC	GGA	CTC	ATA	TAC	336
Thr	Lys	Leu	Ser	Trp	Asn	Glu	Asp	Gly	Thr	Ile	His	Gly	Leu	Ile	Tyr	
100		105					100		105			110				
CAG	GAC	GGG	AAC	CTG	ATA	GTC	CAA	TTC	CCT	GGC	TTG	TAC	TTC	ATC	GTT	384
Gln	Asp	Gly	Asn	Leu	Ile	Val	Gln	Phe	Pro	Gly	Leu	Tyr	Phe	Ile	Val	
115						115		120			125					
TGC	CAA	CTG	CAG	TTC	CTC	GTG	CAG	TGC	TCA	AAT	CAT	TCT	GTG	GAC	CTG	432
Cys	Gln	Leu	Gln	Phe	Leu	Val	Gln	Cys	Ser	Asn	His	Ser	Val	Asp	Leu	
130		135					130		135			140				
ACA	TTG	CAG	CTC	CTC	ATC	AAT	TCC	AAG	ATC	AAA	AAG	CAG	ACG	TTG	GTA	480
Thr	Leu	Gln	Leu	Leu	Ile	Asn	Ser	Lys	Ile	Lys	Lys	Gln	Thr	Leu	Val	
145		150					145		150			155			160	

ACA GTG TGT GAG TCT GGA GTT CAG AGT AAG AAC ATC TAC CAG AAT CTC	528	
Thr Val Cys Glu Ser Gly Val Gln Ser Lys Asn Ile Tyr Gln Asn Leu		
165	170	175
TCT CAG TTT TTG CTG CAT TAC TTA CAG GTC AAC TCT ACC ATA TCA GTC	576	
Ser Gln Phe Leu Leu His Tyr Leu Gln Val Asn Ser Thr Ile Ser Val		
180	185	190
AGG GTG GAT AAT TTC CAG TAT GTG GAT ACA AAC ACT TTC CCT CTT GAT	624	
Arg Val Asp Asn Phe Gln Tyr Val Asp Thr Asn Thr Phe Pro Leu Asp		
195	200	205
AAT GTG CTA TCC GTC TTC TTA TAT AGT AGC TCA GAC TGA	663	
Asn Val Leu Ser Val Phe Leu Tyr Ser Ser Ser Asp		
210	215	220

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 220 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gln Val Gln Pro Gly Ser Val Ala Ser Pro Trp Arg Ser Thr Arg			
1	5	10	15
Pro Trp Arg Ser Thr Ser Arg Ser Tyr Phe Tyr Leu Ser Thr Thr Ala			
20	25	30	
Leu Val Cys Leu Val Val Ala Val Ala Ile Ile Leu Val Leu Val Val			
35	40	45	
Gln Lys Lys Asp Ser Thr Pro Asn Thr Thr Glu Lys Ala Pro Leu Lys			
50	55	60	
Gly Gly Asn Cys Ser Glu Asp Leu Phe Cys Thr Leu Lys Ser Thr Pro			
65	70	75	80
Ser Lys Lys Ser Trp Ala Tyr Leu Gln Val Ser Lys His Leu Asn Asn			
85	90	95	
Thr Lys Leu Ser Trp Asn Glu Asp Gly Thr Ile His Gly Leu Ile Tyr			
100	105	110	
Gln Asp Gly Asn Leu Ile Val Gln Phe Pro Gly Leu Tyr Phe Ile Val			
115	120	125	
Cys Gln Leu Gln Phe Leu Val Gln Cys Ser Asn His Ser Val Asp Leu			
130	135	140	
Thr Leu Gln Leu Leu Ile Asn Ser Lys Ile Lys Lys Gln Thr Leu Val			
145	150	155	160
Thr Val Cys Glu Ser Gly Val Gln Ser Lys Asn Ile Tyr Gln Asn Leu			
165	170	175	

Ser	Gln	Phe	Leu	Leu	His	Tyr	Leu	Gln	Val	Asn	Ser	Thr	Ile	Ser	Val
180								185						190	
Arg	Val	Asp	Asn	Phe	Gln	Tyr	Val	Asp	Thr	Asn	Thr	Phe	Pro	Leu	Asp
195							200						205		
Asn	Val	Leu	Ser	Val	Phe	Leu	Tyr	Ser	Ser	Ser	Asp				
210						215					220				

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein fragment
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: huCD30-L fragment (PRELIM)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Pro	Gly	Asp	Thr	Val	Xaa	His	Val	Pro	Ala	Gly	Ser	Glu	Ala	Ser	His
1				5				10						15	
Leu	Gly	Thr	Thr	Ser	Arg	Xaa	Tyr	Phe	Tyr	Leu	Thr	Thr	Xaa	Thr	Leu
				20				25					30		
Ala	Leu	Cys	Leu	Val	Phe	Thr	Val	Ala	Thr	Ile	Met	Val	Leu	Val	Val
				35				40				45			
Gln	Arg	Thr	Asp	Ser	Ile	Pro	Asn	Ser	Pro	Asp	Asn	Val	Pro	Leu	Lys
				50				55				60			
Gly	Gly	Asn	Cys	Ser	Glu	Asp	Leu	Leu	Cys	Ile	Leu	Lys	Arg	Ala	Pro
				65				70			75		80		
Phe	Lys	Lys	Ser	Trp	Ala	Tyr	Leu	Gln	Val	Xaa	Lys	His	Leu	Asn	Lys
				85					90				95		
Thr	Xaa	Leu	Ser	Trp	Asn	Lys	Asp	Gly	Ile	Leu	His	Gly	Val	Arg	Tyr
				100					105				110		
Gln	Asp	Gly	Asn	Leu	Val	Ile	Gln	Phe	Pro	Gly	Phe	Val			
				115				120				125			

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein fragment

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: muCD30-L fragment (PRELIM)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Gln Val Gln Pro Gly Ser Val Ala Ser Pro Trp Arg Ser Thr Arg
1 5 10 15

Pro Trp Arg Ser Thr Ser Arg Ser Tyr Phe Tyr Leu Ser Thr Thr Ala
20 25 30

Leu Val Cys Leu Val Val Xaa Val Ala Ile Ile Leu Val Leu Val Val
35 40 45

Gln Lys Lys Asp Ser Thr Pro Asn Thr Thr Glu Lys Ala Pro Leu Lys
50 55 60

Gly Gly Asn Cys Ser Glu Asp Leu Phe Cys Thr Leu Lys Ser Thr Pro
65 70 75 80

Ser Lys Lys Ser Trp Ala Tyr Leu Gln Val Ser Lys His Leu Asn Asn
85 90 95

Thr Lys Leu Ser Trp Asn Glu Asp Gly Thr Ile His Gly Leu Ile Tyr
100 105 110

Gln Asp Gly Asn Leu Ile Val Gln Phe Pro Gly Leu Tyr Phe Ile Val
115 120 125

Cys Gln
130

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: huCD30-L

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG CAT GTG CCG GCG TCC GTG GCC AGC CAC CTG GGG ACC ACG AGC Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly Thr Thr Ser	1 5 10 15	48
CGC AGC TAT TTC TAT TTG ACC ACA GCC ACT CTG GCT CTG TGC CTT GTC Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu Cys Leu Val	20 25 30	96
TTC ACG GTG GCC ACT ATT ATG GTG TTG GTC GTT CAG AGG ACG GAC TCC Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg Thr Asp Ser	35 40 45	144
ATT CCC AAC TCA CCT GAC AAC GTC CCC CTC AAA GGA GGA AAT TGC TCA Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly Asn Cys Ser	50 55 60	192
GAA GAC CTC TTA TGT ATC CTG AAA AGA GCT CCA TTC AAG AAG TCA TGG Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys Lys Ser Trp	65 70 75 80	240
GCC TAC CTC CAA GTG GCA AAG CAT CTA AAC AAA ACC AAG TTG TCT TGG Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys Leu Ser Trp	85 90 95	288
AAC AAA GAT GGC ATT CTC CAT GGA GTC AGA TAT CAG GAT GGG AAT CTG Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp Gly Asn Leu	100 105 110	336
GTG ATC CAA TTC CCT GGT TTG TAC TTC ATC ATT TGC CAA CTG CAG TTT Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln Leu Gln Phe	115 120 125	384
CTT GTA CAA TGC CCA AAT AAT TCT GTC GAT CTG AAG TTG GAG CTT CTC Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu Glu Leu Leu	130 135 140	432
ATC AAC AAG CAT ATC AAA AAA CAG GCC CTG GTG ACA GTG TGT GAG TCT Ile Asn Lys His Ile Lys Gln Ala Leu Val Thr Val Cys Glu Ser	145 150 155 160	480
GGA ATG CAA ACG AAA CAC GTA TAC CAG AAT CTC TCT CAA TTC TTG CTG Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln Phe Leu Leu	165 170 175	528
GAT TAC CTG CAG GTC AAC ACC ACC ATA TCA GTC AAT GTG GAT ACA TTC Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val Asp Thr Phe	180 185 190	576
CAG TAC ATA GAT ACA AGC ACC TTT CCT CTT GAG AAT GTG TTG TCC ATC Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val Leu Ser Ile	195 200 205	624
TTC TTA TAC AGT AAT TCA GAC TGA Phe Leu Tyr Ser Asn Ser Asp	210 215	648

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 215 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly Thr Thr Ser
1 5 10 15

Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu Cys Leu Val
20 25 30

Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg Thr Asp Ser
35 40 45

Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly Asn Cys Ser
50 55 60

Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys Lys Ser Trp
65 70 75 80

Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys Leu Ser Trp
85 90 95

Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp Gly Asn Leu
100 105 110

Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln Leu Gln Phe
115 120 125

Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu Glu Leu Leu
130 135 140

Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val Cys Glu Ser
145 150 155 160

Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln Phe Leu Leu
165 170 175

Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val Asp Thr Phe
180 185 190

Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val Leu Ser Ile
195 200 205

Phe Leu Tyr Ser Asn Ser Asp
210 215